

The figure displays a sequence alignment of the TGF β receptor 1 (TGFbR1) protein across multiple species. The alignment covers the entire protein length from approximately position 10 to 390. The sequence is presented as a grid where each row represents a different species. The alignment uses color coding to highlight conservation: green for hydrophobic residues, blue for polar uncharged, red for acidic, and purple for basic. The alignment shows a high degree of conservation, particularly in the signal peptide and the extracellular domain (residues 10-300), while the intracellular kinase domain (residues 300-390) shows more variation.

810 820 830 840 850 860 870 880 890 900 910 920

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27260970.Q
15237373.P
AK101371.Q
AK100827.Q
15238886.P
AK072806.Q
30679773.P
AK067054.Q
AK063305.Q
49010005.Q **KMWGDRER**
15240038.P
AK067283.Q
AK100639.Q
AK071077.Q
AK070226.Q
15232294.P
30696629.P
61980009.Q
61980010.Q
18397825.P
15230190.P
15235623.P
15237361.P **SRYDSGRDHDDSSRNTSMRINSLAHDDKEEDEENHETRSYSDHDDSF**
15232987.P **SRYDSDRDQDEKGK**
42110005.Q
15223033.P
15217992.P
15226901.P
15223024.P
AK102717.Q
15231654.P
AK105569.Q
lir3_IRK
2phk_Phk
lias_TGFbR

RETTPT - ADQRATAAEAKTWGENSERKWP-N - GHGSFDSTNE -
RESSRS - TDRQRAAEAKTWGENSERKWP-N - ARGSFDTNE -
RCPTRNKRDLDPERAVAEAKVWGENWREKRKATN - CGPSFDSTND -
LLALHNGQNNSEADIVHKSSVKLDAHEKQRSGS - GKGSRF -
DREMRVAEAKMWGENWREKRRAAATTSSNAQVSLDSPTETG -
MVAEAKMWGENWREMRVAEAKMWGENWREKRRAB - NGQGSLDSTENG -
INERAVAEAKMWGENWREKRRQSE - QGTSES - NSTG -
ADERALAEANVVEAWRRQEKTSKMR -

ATRQKQKAQIQEKTSHLQGIVAPTEINRL -
SVRQKQMAQIKEKKQAQPGIVAP - KTNKL -

SRYDSGRDHDDSSRNTSMRINSLAHDDKEEDEENHETRSYSDHDDSF - DDAGESGESSLHRTEAKEEEHHISSDH
EEEEEEFAEEKHHTIBHIDS SKY'DDDQS VYFND DDDSGDDNGGS LHRIKS - DVAIDSIKE
EEEEEEADEE

RRRVIVDDARTWAGMNRRGATPPPTP -